RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/849,980B*

INPUT SET: S36789.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

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 1                                          SEQUENCE LISTING
 2
 3    (1)     General Information:
 4
 5    (i) APPLICANT: SANTEN PHARMACEUTICAL CO., LTD.
 6    (ii) TITLE OF INVENTION: Novel Polypeptide Having Water Channel
 7    Activity and DNA sequence
 8    (iii) NUMBER OF SEQUENCES:  2
 9    (iv) CORRESPONDENCE ADDRESS:
10     (A) ADDRESSEE: SANTEN PHARMACEUTICAL CO., LTD.
11     (B) STREET: 9 19 Shimoshinjo 3-chome Higashiyodogawa-Ku
12     (C) CITY: Osaka
13     (D) STATE: Osaka
14     (E) COUNTRY: JAPAN
15     (F) ZIP: 533-0021
16    (v) COMPUTER READABLE FORM:
17     (A) MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB, storage
18     (B) COMPUTER: IBM PS/2 or compatibles
19     (C) OPERATING SYSTEM: WINDOWS 95/97
20     (D) SOFTWARE: Microsoft Word 97
21    (vi) CURRENT APPLICATION DATA:
22     (A) APPLICATION NUMBER:US/09/849,980B
23     (B) FILING DATE: 19-OCT-1999
24     (C) CLASSIFICATION:
25    (vii) PRIOR APPLICATION DATA:
26     (A) APPLICATION NUMBER: PCT/JP98/01371
27     (B) FILING DATE: 27-MAR-1998
28     (C) APPLICATION NUMBER: JP 09-094845
29     (D) FILING DATE: 28-MAR-1997
30    (viii) ATTORNEY/AGENT INFORMATION:
31     (A) NAME: Burton A. Amernick
32     (B) REGISTRATION NUMBER: 24852
33     (C) REFERENCE/DOCKET NUMBER: 1581/00156
34    (ix) TELECOMMUNICATION INFORMATION:
35     (A) TELEPHONE: (202)331-7111
36     (B) TELEFAX: (202)293-6229
37
38    (2) INFORMATION FOR SEQ ID NO: 1:
39
40    (i) SEQUENCE CHARACTERISTICS:
41     (A) LENGTH:342 amino acids
42     (B) TYPE: amino acid
43     (D) TOPOLOGY: linear
44    (ii) MOLECULE TYPE: peptide
45
46    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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PATENT APPLICATION *US/09/849,980B*

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47
48    Met Val Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met
49                    5                    10                   15
50    Val Ser Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys
51                    20                   25                   30
52    Met Val Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met
53                    35                   40                   45
54    Val Phe Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr
55            50                   55                   60
56    Gly Ser Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met
57    65                   70                   75                   80
58    Gly Val His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala
59                    85                   90                   95
60    Val Thr Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe
61                    100                  105                  110
62    Pro Val Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala
63                    115                  120                  125
64    Thr Ile Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly
65            130                  135                  140
66    Gln Leu Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr
67    145                  150                  155                  160
68    Tyr Leu Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala
69                    165                  170                  175
70    Trp Leu Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln
71                    180                  185                  190
72    Glu Asn Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile
73            195                  200                  205
74    Leu Val Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala
75            210                  215                  220
76    Ile Asn Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala
77    225                  230                  235                  240
78    Gly Trp Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val
79                    245                  250                  255
80    Pro Val Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr
81                    260                  265                  270
82    Leu Val Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu
83            275                  280                  285
84    Asp Ser Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met
85            290                  295                  300
86    Gly Ser His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser
87    305                  310                  315                  320
88    Pro Ala Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser
89                    325                  330                  335
90    Met Ala Leu Glu His Phe
91                    340
92
93    (2) INFORMATION FOR SEQ ID NO:2:
94    (i) SEQUENCE CHARACTERISTICS:
95     (A) LENGTH:1258 base pairs
96     (B) TYPE: nucleic acid
97     (C) STRANDEDNESS: double
98     (D) TOPOLOGY: linear
99    (ii) MOLECULE TYPE: cDNA to  mRNA
```

```
100   (vi) ORIGINAL SOURCE:
101    (A) ORGANISM: Homo sapiens
102    (B) TISSUE TYPE: fat tissue
103   (ix) FEATURE:
104    (A) NAME/KEY: exon
105    (B) LOCATION: F173..1198
106    (C) IDENTIFICATION METHOD: by experiment
107    (C) IDENTIFICATION METHOD: by experiment
108   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
109
110   GGCTCTGGAC TGGGGACACA GGGATAGCTG AGCCCCAGCT GGGGGTGGAA GCTGAGCCAG   60
111   GGACAGTCAC GGAGGAACAA GATCAAGATG CGCTGTAACT GAGAAGCCCC CAAGGCGGAG  120
112   GCTGAGAATC AGAGACATTT CAGCAGACAT CTACAAATCT GAAAGACAAA AC ATG GTT  178
113                                                             Met Val
114                                                              1
115   CAA GCA TCC GGG CAC AGG CGG TCC ACC CGT GGC TCC AAA ATG GTC TCC   226
116   Gln Ala Ser Gly His Arg Arg Ser Thr Arg Gly Ser Lys Met Val Ser
117           5                   10                  15
118   TGG TCC GTG ATA GCA AAG ATC CAG GAA ATA CTG CAG AGG AAG ATG GTG   274
119   Trp Ser Val Ile Ala Lys Ile Gln Glu Ile Leu Gln Arg Lys Met Val
120       20                  25                  30
121   CGA GAG TTC CTG GCC GAG TTC ATG AGC ACA TAT GTC ATG ATG GTA TTC   322
122   Arg Glu Phe Leu Ala Glu Phe Met Ser Thr Tyr Val Met Met Val Phe
123   35                  40                  45                  50
124   GGC CTT GGT TCC GTG GCC CAT ATG GTT CTA AAT AAA AAA TAT GGG AGC   370
125   Gly Leu Gly Ser Val Ala His Met Val Leu Asn Lys Lys Tyr Gly Ser
126                   55                  60                  65
127   TAC CTT GGT GTC AAC TTG GGT TTT GGC TTC GGA GTC ACC ATG GGA GTG   418
128   Tyr Leu Gly Val Asn Leu Gly Phe Gly Phe Gly Val Thr Met Gly Val
129                   70                  75                  80
130   CAC GTG GCA GGC CGC ATC TCT GGA GCC CAC ATG AAC GCA GCT GTG ACC   466
131   His Val Ala Gly Arg Ile Ser Gly Ala His Met Asn Ala Ala Val Thr
132                   85                  90                  95
133   TTT GCT AAC TGT GCG CTG GGC CGC GTG CCC TGG AGG AAG TTT CCG GTC   514
134   Phe Ala Asn Cys Ala Leu Gly Arg Val Pro Trp Arg Lys Phe Pro Val
135       100                 105                 110
136   TAT GTG CTG GGG CAG TTC CTG GGC TCC TTC CTG GCG GCT GCC ACC ATC   562
137   Tyr Val Leu Gly Gln Phe Leu Gly Ser Phe Leu Ala Ala Ala Thr Ile
138   115                 120                 125                 130
139   TAC AGT CTC TTC TAC ACG GCC ATT CTC CAC TTT TCG GGT GGA CAG CTG   610
140   Tyr Ser Leu Phe Tyr Thr Ala Ile Leu His Phe Ser Gly Gly Gln Leu
141                   135                 140                 145
142   ATG GTG ACC GGT CCC GTC GCT ACA GCT GGC ATT TTT GCC ACC TAC CTT   658
143   Met Val Thr Gly Pro Val Ala Thr Ala Gly Ile Phe Ala Thr Tyr Leu
144                   150                 155                 160
145   CCT GAT CAC ATG ACA TTG TGG CGG GGC TTC CTG AAT GAG GCG TGG CTG   706
146   Pro Asp His Met Thr Leu Trp Arg Gly Phe Leu Asn Glu Ala Trp Leu
147               165                 170                 175  .
148   ACC GGG ATG CTC CAG CTG TGT CTC TTC GCC ATC ACG GAC CAG GAG AAC   754
149   Thr Gly Met Leu Gln Leu Cys Leu Phe Ala Thr Thr Asp Gln Glu Asn
150       180                 185                 190
151   AAC CCA GCA CTG CCA GGA ACA GAG GCG CTG GTG ATA GGC ATC CTC GTG   802
152   Asn Pro Ala Leu Pro Gly Thr Glu Ala Leu Val Ile Gly Ile Leu Val
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153    195                        200                      205                        210
154    GTC ATC ATC GGG GTG TCC CTT GGC ATG AAC ACA GGA TAT GCC ATC AAC       850
155    Val Ile Ile Gly Val Ser Leu Gly Met Asn Thr Gly Tyr Ala Ile Asn
156                       215                      220                      225
157    CCG TCC CGG GAC CTG CCC CCC CGC ATC TTC ACC TTC ATT GCT GGT TGG       898
158    Pro Ser Arg Asp Leu Pro Pro Arg Ile Phe Thr Phe Ile Ala Gly Trp
159                   230                      235                      240
160    GGC AAA CAG GTC TTC AGC AAT GGG GAG AAC TGG TGG TGG GTG CCA GTG       946
161    Gly Lys Gln Val Phe Ser Asn Gly Glu Asn Trp Trp Trp Val Pro Val
162               245                      250                      255
163    GTG GCA CCA CTT CTG GGT GCC TAT CTA GGT GGC ATC ATC TAC CTG GTC       994
164    Val Ala Pro Leu Leu Gly Ala Tyr Leu Gly Gly Ile Ile Tyr Leu Val
165        260                      265                      270
166    TTC ATT GGC TCC ACC ATC CCA CGG GAG CCC CTG AAA TTG GAG GAT TCT      1042
167    Phe Ile Gly Ser Thr Ile Pro Arg Glu Pro Leu Lys Leu Glu Asp Ser
168    275                      280                      285                      290
169    GTG GCG TAT GAA GAC CAC GGG ATA ACC GTA TTG CCC AAG ATG GGA TCT      1090
170    Val Ala Tyr Glu Asp His Gly Ile Thr Val Leu Pro Lys Met Gly Ser
171                   295                      300                      305
172    CAT GAA CCC ACG ATC TCT CCC CTC ACC CCC GTC TCT GTG AGC CCT GCC      1138
173    His Glu Pro Thr Ile Ser Pro Leu Thr Pro Val Ser Val Ser Pro Ala
174               310                      315                      320
175    AAC AGA TCT TCA GTC CAC CCT GCC CCA CCC TTA CAT GAA TCC ATG GCC      1186
176    Asn Arg Ser Ser Val His Pro Ala Pro Pro Leu His Glu Ser Met Ala
177               325                      330                      335
178    CTA GAG CAC TTC TAAGCAGAGA TTATTTGTGA TCCCATCCAT TCCCCAATAA         1238
179    Leu Glu His Phe
180        340
181    AGCAAGGCTT GTCCGACAAA                                               1258
182
183
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/09/849,980B*

INPUT SET: S36789.raw

Line	Error	Original Text
22	Wrong application Serial Number	(A) APPLICATION NUMBER:US/09/849,980B